Curriculum Vitae

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CONTACT INFORMATION

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RESEARCH INTERESTS

Longitudinal data analysis; Varying coefficient models; Mixed effects models; Kernel machine methods; Mediation analysis; Machine learning methods; Network analysis; Whole genome sequencing; Bulk and single-cell RNA sequencing; Spatial transcriptomics; Biomarker studies; Electronic health records

EDUCATION

University of Science & Technology of China, Hefei, Anhui, China
B.S. in Biology, July 2001

University of Florida, Gainesville, FL
M.S. in Statistics, August 2004

University of Chicago, Chicago, IL
Ph.D. in Statistics, August 2009

PROFESSIONAL POSITIONS

- Assistant Professor, Department of Biostatistics, Yale School of Public Health, 2009–2016
- Associate Professor (with Term), Department of Biostatistics, Yale School of Public Health, 2016–2020
- Associate Professor (with Tenure), Department of Biostatistics, Yale School of Public Health, 2020–present
- Affiliated Faculty, Computational Biology and Bioinformatics Program, Yale School of Medicine, 2012–present
- Affiliated Faculty, Department of Biomedical Informatics & Data Science, Yale School of Medicine, 2024–present
- Member, Center for Biomedical Data Science, Yale School of Medicine, 2019–present
- Member, Genomics, Genetics, and Epigenetics Program, Yale Cancer Center, 2020–present

- Member, Center for Brain and Mind Health, Yale School of Medicine, 2023–present

HONORS AND AWARDS

- Yale School of Public Health Faculty Marshal, University Commencement, 2022.
- Feature Nomination, Society for Mathematical Biology (SMB) Diversity, Equity and Inclusion, 2021.
- Elected Member, International Statistical Institute (ISI), 2015.
- Institute of Mathematical Statistics (IMS) New Researchers Conference Travel Award, 2013.
- Yale Center for Clinical Investigation Scholar Award, 2012.
- Eastern North American Region (ENAR) Junior Investigator Workshop Travel Award, 2012.
- International Genetic Epidemiology Society (IGES) Meeting Travel Award, 2007.
- Paul Meier Fellowship, Department of Statistics, University of Chicago, 2004.
- Member, Mu Sigma Rho National Statistics Honorary Society, 2004
- International Student Academic Award, Office of International Studies and Programs, University of Florida, 2004.
- William Mendenhall Award for outstanding first year graduate student, Department of Statistics, University of Florida, 2003.
- International Student Academic Award, Office of International Studies and Programs, University of Florida, 2003.

BIBLIOGRAPHY

(* Co-first author; † Co-senior author)

Peer-Reviewed Original Research

1. Lou X.Y., Todhunter R.J., Lin M., Lu Q., Liu T., **Wang Z.**, Bliss S.P., Casella G., Acland G.M., Lust G., Wu R., (2003) The extent and distribution of linkage disequilibrium in a multi-hierarchic outbred canine pedigree. *Mammalian Genome*, 14:555-564.
2. Wu R., Ma C.X., Lin M., **Wang Z.**, Casella G., (2004) Functional mapping of quantitative trait loci underlying growth trajectories using a transform-both-sides logistic model. *Biometrics*, 60:729-738.
3. Gong Y.*, **Wang Z.***, Liu T., Zhao W., Zhu Y., Johnson J.A., Wu R., (2004) A statistical model for functional mapping of quantitative trait loci regulating drug response. *The Pharmacogenomics Journal*, 4:315-321.
4. **Wang Z.**, Wu R., (2004) A statistical model for high-resolution mapping of quantitative trait loci determining HIV dynamics. *Statistics in Medicine*, 23:3033-3051.
5. Wu R., **Wang Z.**, Zhao W., Cheverud J.M., (2004) A mechanistic model for genetic machinery of ontogenetic growth. *Genetics*, 168:2383-2394.

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8. **Wang Z.**, McPeek M.S., (2009) An incomplete-data quasi-likelihood approach to haplotype-based genetic association studies on related individuals. *Journal of the American Statistical Association*, 104:1251-1260.
9. **Wang Z.**, McPeek M.S., (2009) ATRIUM: Testing untyped SNPs in case-control association studies with related individuals. *American Journal of Human Genetics*, 85:667-678.
10. Huang J., Detterbeck F.C., **Wang Z.**, Loehrer P.J. Sr., (2010) Standard outcome measures for thymic malignancies. *Journal of Thoracic Oncology*, 5:2017-2023.
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12. Wang K., Li W.D., Zhang C.K., **Wang Z.**, Glessner J.T., Grant S.F.A., Zhao H., Hakonarson H., Price R.A., (2011) A genome-wide association study on obesity and obesity-related traits. *PLoS One*, 6:e18939.
13. Wu C., DeWan A., Hoh J., **Wang Z.**, (2011) A comparison of association methods correcting for population stratification in case-control studies. *Annals of Human Genetics*, 75:418-427.
14. Huang J., Detterbeck F.C., **Wang Z.**, Loehrer P.J. Sr., (2011) Standard outcome measures for thymic malignancies. *Journal of Thoracic Oncology*, 6:S1691-S1697. **This article was translated in Chinese and published at Chinese Journal of Lung Cancer, 2014, 17:122-129.*
15. Muralidaran A., Detterbeck F.C., Boffa D.J., **Wang Z.**, Kim A.W., (2011) Long-term survival after lung resection for non-small cell lung cancer with circulatory bypass: a systematic review. *Journal of Thoracic and Cardiovascular Surgery*, 142:1137-1142.
16. Wu C., Walsh K.M., DeWan A.T., Hoh J., **Wang Z.**, (2011) Disease risk prediction with rare and common variants. *BMC Proceedings*, 5:S61.
17. Kim A.W., Boffa D.J., **Wang Z.**, Detterbeck F.C., (2012) An analysis, systematic review, and meta-analysis of the perioperative mortality after neoadjuvant therapy and pneumonectomy for non-small cell lung cancer (NSCLC). *Journal of Thoracic and Cardiovascular Surgery*, 143:55-63.
18. Zhang C.K., Stein P.B., Liu J., **Wang Z.**, Yang R., Cho J.H., Gregersen P.K., Aerts J.M., Zhao H., Pastores G.M., Mistry P.K., (2012) Genome-wide association study of N370S homozygous Gaucher disease reveals the candidacy of CLN8 gene as a genetic modifier contributing to extreme phenotypic variation. *American Journal of Hematology*, 87:377-383.

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23. **Wang Z.**, Luo J., Fu G., Wang Z., Wu R., (2013) Stochastic modeling of systems mapping in pharmacogenomics. *Advanced Drug Delivery Reviews*, 65:912-917.
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78. Shan N., Xie Y., Song S., Jiang W., **Wang Z.**[†], Hou L.[†], (2021) A novel transcriptional risk score for risk prediction of complex human diseases. *Genetic Epidemiology*, 45:811-820.
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Zhao D., Ijaz S., Sakai C., Szi C., Rooney B., Ghosh M., Nwabudike I., Gorodezky A., Chowdhury S., Zaheer M., McLaughlin S., Fernandez J.M., Wu J., Eilbott J.A., Vander Wyk B., Rihel J., Papademetris X., **Wang Z.**, Hoffman E.J., (2023) High-throughput functional analysis of autism genes in zebrafish identifies convergence in dopaminergic and neuroimmune pathways. *Cell Reports*, 42:112243.

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95. Zhang B., Wang S., Luo Y., Chiu C.-Y., Xu G., Ding J., Amei A., **Wang Z.**, Wilson A.F., Bailey-Wilson J.E., Xiong M., Fan R., (2025) Stochastic generalized functional linear models for gene-based association analysis of binary traits in longitudinal studies. *Statistics and Its Interface*, 18:177-188.
96. Huang X., Arora J., Erzurumluoglu A.M., Stanhope S.A., Lam D., Boehringer Ingelheim-Global Computational Biology and Digital Sciences, Zhao H., Ding Z., **Wang Z.**†, de Jong J.†, (2025) Enhancing patient representation learning with inferred family pedigrees improves disease risk prediction. *Journal of the American Medical Informatics Association*, ocae297.
97. Korutla L., Hu R., Liu Y., Romano C., Habertheuer A., Abedi P., Wang H., Molugu S., Rostami S., Naji A., Marguiles K., Nuqali A., Beasley M., Maulion C., Hahn S., Ahmad T., **Wang Z.**, Sen S., Vallabhajosyula P., (2025) Circulating tissue specific extracellular vesicles for noninvasive monitoring of acute cellular rejection in clinical heart transplantation. *Transplantation*, in press.

Chapters

98. **Wang Z.**, Yan X., (2022) Computational and statistical methods for single-cell RNA sequencing data. In: Lu H.H.-S., Schölkopf B., Wells M.T., Zhao H., (eds), Handbook of Statistical Bioinformatics, 2nd Ed., Springer Handbooks of Computational Statistics. Springer, Berlin, Heidelberg. pp 3-35.

Commentaries, Editorials, and Letters

99. Wu R., **Wang Z.**, (2013) Mathematical modeling of systems pharmacogenomics towards personalized drug delivery. *Advanced Drug Delivery Reviews*, 65:903-904.
100. **Wang Z.**, (2017) Integrating evolutionary game theory into epigenetic study of embryonic development: Comment on "Epigenetic game theory: How to compute the epigenetic control of maternal-to-zygotic transition" by Qian Wang et al. *Physics of Life Reviews*, 20:164-165.

Manuscripts Under Revision

1. Wang S., Luo Y., Chiu C.-Y., Xu G., Amei A., Zhang J., **Wang Z.**, Fang H.-B., Wilson A.F., Bailey-Wilson J.E., Fan R., Bivariate stochastic functional linear models for gene-based association analysis of quantitative traits in longitudinal studies.
2. Liu Y., **Wang Z.**, Collins S., Testani J., Safdar B., Sex differences in proteomics of cardiovascular disease - results from the Yale-CMD registry.
3. Zhou X., **Wang Z.**, SRD: Sparse ramp discrimination for classification and variable selection on high-dimensional biological data.

4. Garcia M.F., Retallick-Townsley K., Pruitt A., Davidson E., Dai Y., Fitzpatrick S.E., Sen A., Cohen S., Livoti O., Khan S., Dossou G., Cheung J., Deans P.J.M., **Wang Z.**, Huckins L.M., Hoffman E., Brennand K.J., Dynamic convergence of autism disorder risk genes across neurodevelopment.
`https://doi.org/10.1101/2024.08.23.609190`

Manuscripts Submitted

1. Xiao X., Zhang L., Zhao H., **Wang Z.**, Towards spatial single-cell-level interaction inference: interpreting correlation of cell state and niche learned by self-supervised graph transformer.
2. Xu G., Zhou X., Wang M., Zhang B., Jiang W., Laden F., Suh H.H., Szpiro A.A., Spiegelman D., **Wang Z.**, Causal inference with double/debiased machine learning for evaluating the health effects of multiple mismeasured pollutants.
`https://doi.org/10.48550/arXiv.2410.07135`
3. Kay S., Rajeevan H., Son M., Kwah J., Ramirez M., Liu Y., **Wang Z.**, Yan X., Nino G., Britto C., Chupp G., Gomez J.L., Sex-biased gene expression underlies immune dysfunction in asthma.
4. Zielonka J., Li N., Liu Y., Yan X., **Wang Z.**, Ramirez M., Figueroa A., Korde A., Yin H., Britto C., Singh I., Sun H., Herzog E., Hinchcliff M., Ryu C., Gomez J.L., A cutaneous signature of systemic sclerosis associated with severe skin and pulmonary involvement.
5. Valizadeh A., Zhang X., Roache J.D., Hu Y., Gueorguieva R., Averill L.A., Ranganathan M., **Wang Z.**, Williamson D.E., Shiroma P.R., Girgenti M.J., Petrakis I., López-Roca A.L., Young-McCaughan S.B., Keane T.M., Peterson A.L., Abdallah C.G., Krystal J.H., Xu K., Consortium to Alleviate PTSD, DNA methylation biomarkers predict ketamine response among veterans and active-duty military with PTSD.
6. Aslan M., Tylee D.S., Chen P., Dai Y., Li Y., Mutalik P., Yan L., **Wang Z.**, Polimanti R., Mohamed S., Trends in treatment of major depression at the Veterans Health Administration from 2011 to 2022.

PRESENTATIONS

Invited Talks

- Vanderbilt University, Department of Biostatistics, Nashville, TN. Enhancing patient representation learning with inferred family relations improves disease risk prediction in electronic health records and biobank data. October 2024.
- Joint Statistical Meetings (JSM), Portland, OR. Double/debiased machine learning for causal inference in the presence of measurement error in the exposure of interest and confounders. August 2024.
- New England Statistics Symposium (NESS), Storrs, CT. Enhancing patient representation learning from electronic health records through predicted family relations. May 2024.

- VA Connecticut Healthcare System, Cooperative Studies Program Clinical Epidemiology Research Center Strategic Retreat, West Haven, CT. Representation learning on electronic health records using pedigree-based graph attention networks. October 2023.
- Joint Statistical Meetings (JSM), Toronto, ON, Canada. Graphical generative model for identification of disease associated perturbations to intercellular communications in single-cell RNA sequencing data. August 2023.
- Banff International Research Station (BIRS) Workshop on Data Science Challenges in Single-Cell Research, Banff, AB, Canada. Graphical generative model for identification of disease associated perturbations to intercellular communications in single-cell RNA sequencing data. July 2023.
- ICSA China Conference, Chengdu, Sichuan, China. A hybrid machine learning and regression method for cell type deconvolution in spatial transcriptomics. July 2023.
- New England Statistics Symposium (NESS), Boston, MA. A hybrid machine learning and regression method for cell type deconvolution in spatial transcriptomics. June 2023.
- Joint Statistical Meetings (JSM), Washington, DC. A hybrid machine learning and regression method for cell type deconvolution in spatial transcriptomics. August 2022.
- ICSA China Conference, online. Retrospective varying coefficient association analysis of longitudinal binary traits. July 2022.
- Boehringer Ingelheim, online. Statistical methods for correlated data: application in genetics and genomics. January 2022.
- Joint Statistical Meetings (JSM), online. Variant-set retrospective association tests for longitudinal phenotypes. August 2020.
- University of Nevada, Department of Mathematical Sciences, Las Vegas, NV. Gene graph-based imputation for scRNA-seq data. November 2019.
- ICSA China Conference, Tianjin, China. Retrospective association testing for longitudinal binary outcomes. July 2019.
- Tsinghua University, Center for Statistical Science, Beijing, China. Retrospective association testing for longitudinal binary outcomes. June 2019.
- International Conference on Econometrics and Statistics (EcoSta), Taichung, Taiwan. Identification of trans-eQTLs using mediation analysis with multiple mediators. June 2019.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Raleigh, NC. Identification of trans-eQTLs using mediation analysis with multiple mediators. June 2019.
- New England Statistics Symposium (NESS), Hartford, CT. Identification of trans-eQTLs using mediation analysis with multiple mediators. May 2019.
- University of North Texas, Department of Mathematics, Denton, TX. Retrospective association testing for longitudinal binary outcomes. December 2018.

- Huazhong University of Science and Technology, Wuhan, Hubei, China. Genome-wide association analysis with longitudinal phenotypes. May 2018.
- Shanghai Jiao Tong University, SJTU-Yale Joint Center for Biostatistics, Shanghai, China. Kernel machine association testing in longitudinal studies. April 2018.
- Tsinghua University, Center for Statistical Science, Beijing, China. Mathematical modeling of dendritic cell population dynamics in the immune system. December 2017.
- Beijing University of Technology, Department of Probability and Statistics, Beijing, China. Joint statistical modeling of multiple phenotypes in samples with related individuals. December 2017.
- Johns Hopkins University, Research Program in Quantitative Sciences, Division of Biostatistics & Bioinformatics at the SKCCC. Baltimore, MD. Kernel machine association testing in longitudinal studies. September 2017.
- ICSA China Conference: with focus on lifetime data. Jilin, Changchun, China. GEE-based kernel machine association testing in longitudinal studies. July 2017.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Chicago, IL. Kernel machine association testing in longitudinal studies. June 2017.
- Conference on Lifetime Data Science: Data Science, Precision Medicine, and Risk Analysis with Lifetime Data. Storrs, CT. Kernel machine association testing in longitudinal studies. May 2017.
- Hong Kong Baptist University, Department of Mathematics, Hong Kong, China. Kernel machine association testing in longitudinal studies. April 2017.
- Pennsylvania State University, Department of Public Health Sciences, Hershey, PA. Kernel machine association testing in longitudinal studies. March 2017.
- The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, Shanghai, China. Longitudinal SNP-set association analysis of quantitative phenotypes. December 2016.
- Tsinghua University, Center for Statistical Science, Beijing, China. Joint statistical modeling of multiple phenotypes in related samples. December 2016.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Atlanta, GA. Kernel machine association testing for longitudinally-measured quantitative phenotypes. June 2016.
- University of Connecticut, Department of Statistics, Storrs, CT. Longitudinal SNP-set association analysis of quantitative phenotypes. February 2016.
- International Symposium on Frontiers of Genetics and Genomics, Shenzhen, Guangdong, China. Genome-wide and epigenome-wide association study in an HIV cohort. December 2015.
- VA Connecticut Healthcare System, Cooperative Studies Program Biostatistics Seminar, West Haven, CT. Kernel methods for association testing in longitudinal genetic study of alcohol use disorder in a veteran cohort. November 2015.

- University of Nevada, Department of Mathematical Sciences, Las Vegas, NV. Mathematical modeling of dendritic cell population dynamics in the immune system. October 2015.
- 4th Annual Thomas Ten Have Symposium on Statistics in Psychiatry, New York, NY. A kernel-machine statistical approach to association testing in longitudinal genetic study of alcohol use disorder in a veteran cohort. May 2015.
- Beijing Forestry University, Center for Computational Biology, Beijing, China. Longitudinal exome-focused GWAS of alcohol use disorder in a veteran cohort. December 2014.
- University of Pennsylvania, Department of Biostatistics & Epidemiology, Philadelphia, PA. Kernel methods for association testing in longitudinal genetic study of alcohol use disorder in a veteran cohort. November 2014.
- International Chinese Statistical Association-Korean International Statistical Society (ICSA-KISS) Joint Applied Statistics Symposium, Portland, OR. Longitudinal exome-focused GWAS of alcohol use disorders in a veteran cohort. June 2014.
- Institute of Mathematical Statistics (IMS) New Researchers Conference, Montreal, QC, Canada. A powerful model for family-based case-control studies of genetic imprinting. August 2013.
- Tongji Medical College, Wuhan, Hubei, China. VACS exome chip data analysis. July 2013.
- 4th Institute of Mathematical Statistics (IMS)-China International Conference, Chengdu, Sichuan, China. Joint statistical modeling of multiple phenotypes in related samples. July 2013.
- Huazhong University of Science and Technology, Wuhan, Hubei, China. Stochastic modeling of systems mapping in pharmacogenomics. June 2013.
- The Western North American Region of the International Biometric Society (WNAR) Annual Meeting, Los Angeles, CA. Joint statistical modeling of multiple phenotypes in related samples. June 2013.
- Stony Brook University, Stony Brook, NY. Joint statistical modeling of multiple phenotypes in related samples. May 2013.
- 2nd Annual Thomas Ten Have Symposium on Statistics in Psychiatry, New York, NY. Joint statistical modeling of multiple phenotypes in related samples. May 2013.
- University of Guelph, Department of Mathematics & Statistics, Guelph, ON, Canada. Direct assessment of multiple testing correction in genetic association studies with related individuals. November 2012.
- International Symposium on Mapping the Genetic Regulation of Forest Ecosystems, Beijing, China. Joint statistical modeling of multiple phenotypes in related samples. October 2012.
- Zhejiang A & F University, Lin'an, Hangzhou, Zhejiang, China. A powerful association test of ordinal traits in samples with related individuals. July 2012.

- Beijing Forestry University, Center for Computational Biology, Beijing, China. Quasi-likelihood methods and association analysis with related samples. July 2012.
- Beijing Computing Institute, Beijing, China. Genome-wide association studies and assessment of the risk of disease. July 2012.
- 2nd Joint Biostatistics Symposium, Beijing, China. Joint statistical modeling of multiple phenotypes in related samples. July 2012.
- International Conference and Exhibition on Biometrics & Biostatistics, Omaha, NE. A powerful model for family-based case-control studies of genetic imprinting. March 2012.
- Beijing Computing Institute, Beijing, China. Genome-wide association studies, disease risk prediction, and application in biology and medicine. August 2011.
- International Symposium on Genome-Wide Association Studies, Beijing, China. Direct assessment of multiple testing correction in case-control association studies with related individuals. August 2011.
- Beijing University of Technology, Department of Probability and Statistics, Beijing, China. Direct assessment of multiple testing correction in case-control association studies with related individuals. July 2011.
- International Chinese Statistical Association (ICSA) Applied Statistics Symposium, New York, NY. A powerful association test of ordinal traits in samples with related individuals. June 2011.
- France Chicago Collaborating in the Sciences (FACCTS) Workshops, Chicago, IL. Haplotype-based case-control association testing with related individuals: application to analysis of untyped SNPs. May 2009.
- University of Minnesota, Division of Biostatistics, Minneapolis, MN. Testing untyped SNPs in case-control association studies with related individuals. April 2009.
- Columbia University, Department of Biostatistics, New York City, NY. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- Genentech, Inc, South San Francisco, CA. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- University of California at Riverside, Department of Statistics, Riverside, CA. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- St. Jude Children's Research Hospital, Department of Biostatistics, Memphis, TN. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- University of Chicago, Department of Human Genetics, Chicago, IL. Haplotype-based case-control association testing with related individuals. February 2009.
- Yale University, Department of Epidemiology and Public Health, New Haven, CT. Testing untyped SNPs in case-control association studies with related individuals. February 2009.

- Michigan Technological University, Department of Mathematical Sciences, Houghton, MI. Testing untyped SNPs in case-control association studies with related individuals. January 2009.

Peer-reviewed Talks

- American Medical Informatics Association (AMIA) Informatics Summit, Boston, MA. GATEHR: representation learning on electronic health records using pedigree-based graph attention networks. March 2024.
- Asia Pacific Bioinformatics Conference (APBC), Wuhan, Hubei, China. Identification of trans-eQTLs using mediation analysis with multiple mediators. January 2019.
- Joint Statistical Meetings (JSM), Chicago, IL. Kernel machine statistical approaches to genetic association testing in longitudinal studies. August 2016.
- Joint Statistical Meetings (JSM), Seattle, WA. A novel kernel-based statistical approach to testing association with body mass index in a longitudinal genetic study. August 2015.
- Joint Statistical Meetings (JSM), Montreal, QC, Canada. Stochastic modeling of systems mapping in pharmacogenomics. August 2013.
- Joint Statistical Meetings (JSM), San Diego, CA. Improved statistical methods for allele frequency estimation in sequencing data. July 2012.
- Joint Statistical Meetings (JSM), Vancouver, BC, Canada. Multiple testing correction method in genetic association studies with related individuals. August 2010.
- The Eastern North American Region of the International Biometric Society (ENAR) Meeting, New Orleans, LA. Association analysis of ordinal traits on related individuals. March 2010.
- The Eastern North American Region of the International Biometric Society (ENAR) Meeting, Arlington, VA. An incomplete-data quasi-likelihood framework with application to genetic association studies on related individuals. March 2008.
- Genentech, Inc, South San Francisco, CA. Designing a single arm phase II clinical trial with time to event endpoint. August 2004.
- The Eastern North American Region of the International Biometric Society (ENAR) Meeting, Pittsburgh, PA. A unifying model for fine mapping of quantitative trait loci affecting CD4$^+$ T cell and HIV-1 dynamics under highly active antiretroviral therapy. March 2004.

Posters

- American Society of Human Genetics (ASHG) Annual Meeting, Denver, CO. Integrating clinical and genetic data into graph attention networks for disease risk prediction using Biobank data. November 2024.
- American Society of Human Genetics (ASHG) Annual Meeting, Los Angeles, LA. A hybrid machine learning and regression method for cell type deconvolution of spatial barcoding-based transcriptomic data. October 2022.

- American Society of Human Genetics (ASHG) Annual Meeting, Houston, TX. Longitudinal variant-set retrospective association test. October 2019.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Houston, TX. Identification of trans-eQTLs using mediation analysis with multiple mediators. October 2019.
- American Society of Human Genetics (ASHG) Annual Meeting, San Diego, CA. Retrospective association tests for longitudinal binary outcomes in GWAS. October 2018.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Cambridge, UK. Joint statistical modeling of multiple phenotypes in related samples. September 2017.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Baltimore, MD. Kernel machine association testing for longitudinally-measured quantitative phenotypes. October 2015.
- 37th Annual Research Society on Alcoholism (RSA) Scientific Meeting, San Antonio, TX. A novel kernel-based statistical approach to testing association with body mass index in a longitudinal genetic study. June 2015.
- International Genetic Epidemiology Society (IGES) Annual Meeting, Vienna, Austria. Longitudinal exome-focused GWAS of alcohol use disorder in a veteran cohort. August 2014.
- American Society of Human Genetics (ASHG) Annual Meeting, San Francisco, CA. Joint statistical modeling of multiple phenotypes in samples with related individuals. November 2012.
- American Society of Human Genetics (ASHG) Annual Meeting, Montreal, QC, Canada. A powerful model for family-based case-control studies of genetic imprinting. October 2011.
- 2nd Midwest Statistics Research Colloquium, Chicago, IL. Testing untyped SNPs in case-control association studies with related individuals. March 2009.
- 1st Midwest Statistics Research Colloquium, Chicago, IL. An incomplete-data quasi-likelihood framework with application to genetic association studies on related individuals. March 2008.
- International Genetic Epidemiology Society (IGES) Annual Meeting, York, England, UK. Haplotype-based case-control association studies with related individuals: a quasi-likelihood score test approach. September 2007.
- SNPs, Haplotypes, and Cancer: Applications in Molecular Epidemiology Meeting, AACR, Key Biscayne, FL. A dynamic model for genetic control of tumor growth. September 2003.

PROFESSIONAL SERVICE

Peer Review Groups/Grant Study Sections

- Member, Lion Heart Grant Review Committee, 2024
- Ad Hoc Member, MCB-GM Review Panel, NSF, 2024

- Grant Reviewer, Ministry of Health, Singapore, 2022
- Grant Reviewer, National Science Centre, Poland, 2020
- Member, Joint DMS/NIGMS Review Panel, NSF, 2019
- Grant Reviewer, Nebraska Research Initiative, 2017
- Grant Reviewer, Israel Science Foundation, 2016

Editorial Service

- Associate Editor, *Statistics Innovation*, 2024–present
- Associate Editor, *Frontiers in Systems Biology, Section on Integrative Genetics and Genomics*, 2023–present
- Associate Editor, *BMC Genomics*, 2020–present
- Associate Editor, *BMC Genetics*, 2012–2020
- Theme Co-Editor, Mathematical modeling of systems pharmacogenomics, special issue of *Advanced Drug Delivery Reviews*, 2012

Journal Referee

American Journal of Human Genetics; *Annals of Applied Statistics*; *Atherosclerosis*; *Bioinformatics*; *Biostatistics*; *BMC Genetics*; *Briefings in Bioinformatics*; *Cell Reports Methods*; *Frontiers in Bioscience*; *Frontiers in Genetics*; *Genetic Epidemiology*; *Genetics*; *Genomics*; *Human Genetics*; *Human Heredity*; *Human Molecular Genetics*; *Infection, Genetics and Evolution*; *International Journal of Data Mining and Bioinformatics*; *Journal of Biometrics & Biostatistics*; *Journal of Biopharmaceutical Statistics*; *Journal of Computational Biology*; *Journal of the American Statistical Association*; *Ornamental Plant Research*; *Pharmacogenomics*; *Plant Biotechnology Journal*; *PLoS Computational Biology*; *PLoS Genetics*; *PLoS One*; *Proceedings of the National Academy of Sciences of the United States of America*; *Quantitative Biology*; *Scientific Reports*; *Statistical Applications in Genetics and Molecular Biology*; *Statistics and Its Interface*; *Statistics in Biosciences*; *Statistics in Medicine*; *Theranostics*; *International Conference on Research in Computational Molecular Biology (RECOMB 2020)*

Society Activities

- Chair, Student Poster Award Competition, New England Statistics Symposium (NESS), 2025
- Member, Nomination Committee in Bioinformatics, Frontiers of Science Award (FSA), International Congress of Basic Science (ICBS), 2024
- Judge, Student Poster Award Competition, New England Statistics Symposium (NESS), 2024
- Member, Communications Committee, International Genetic Epidemiology Society (IGES), 2019–present
- Reviewer, Student Paper Award Competition, Section on Statistics in Genomics and Genetics, American Statistical Association (ASA), 2017
- Reviewer, Student Paper Award Competition, Section on Statistics in Genomics and Genetics, American Statistical Association (ASA), 2016

- President, American Statistical Association (ASA), Connecticut Chapter, 2014–2015
- Organizing Committee, Thomas R. Ten Have Symposium on Statistics in Mental Health, 2022–present
- Scientific Program Committee, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2025
- Program Committee, New England Statistics Symposium (NESS), 2025
- Organizer, Empowering Precision Medicine with Statistical and Machine Learning Insights Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2025
- Organizer, Recent Developments in Statistics and Machine Learning for Electronic Health Records Data and Precision Medicine Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2024
- Organizer, Recent Advances in Analysis of Large-Scale Omics Data Session, Joint Statistical Meetings (JSM), 2023
- Organizer, Statistical and Machine Learning Methods in Omics Data Analysis Session, New England Statistics Symposium (NESS), 2023
- Organizer, Statistical Advance and Computational Challenges in Omics Studies Session, International Chinese Statistical Association (ICSA) China Conference, 2019
- Organizer, Statistical Advances in Genetics, Genomics and Bioinformatics Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2019
- Organizer, Recent Advance in Bioinformatics and Computational Biology Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2017
- Organizer, Advance in Statistical Genomics and Computational Biology Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2016
- Organizer, Recent Advances in Genetic Epidemiology Session, New England Statistics Symposium (NESS), 2016
- Chair, Challenging Statistical Issues in Functional Neuroimaging Modeling Session, 4th Institute of Mathematical Statistics (IMS)-China international conference, 2013
- Organizer, Statistical Challenges in Large Scale Genetic Studies of Complex Diseases Session, The Eastern North American Region of the International Biometric Society (ENAR) Meeting, 2013
- Chair, Statistical Genomics Session, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2011

Yale University Services

- Chair, Faculty Search Committee, Department of Biostatistics, Yale School of Public Health, 2024–2025
- Member, Faculty Search Committee, Department of Biostatistics, Yale School of Public Health, 2021–2022
- COVID-19 Safety Officers, Yale School of Public Health, 2020

- Member, Selection Committee on YSPH Associate Dean for Diversity, Equity and Inclusion, Yale School of Public Health, 2019
- Member, MPH Admissions Committee, Yale School of Public Health, 2017–2022
- Member, Practicum Advisory Committee (PAC), Yale School of Public Health, 2015–2017
- Member, Committee on Academic and Professional Integrity (CAPI), Yale School of Public Health, 2012–2015
- Member, Faculty Search Committee, Department of Biostatistics, Yale School of Public Health, 2012–2013
- Chair, Qualifying Exam Committee, Department of Biostatistics, Yale School of Public Health, 2021–present
- Chair, Colin White Memorial Scholarship Committee, Department of Biostatistics, Yale School of Public Health, 2019–2022
- Member, Qualifying Exam Committee, Department of Biostatistics, Yale School of Public Health, 2019–2020
- Chair, Master Thesis Prize Committee, Department of Biostatistics, Yale School of Public Health, 2013–present
- Member, Colin White Memorial Scholarship Committee, Department of Biostatistics, Yale School of Public Health, 2012–2018
- Department Seminar Organizer, Department of Biostatistics, Yale School of Public Health, 2012
- Department Seminar Organizer, Department of Biostatistics, Yale School of Public Health, 2009–2010

TEACHING ACTIVITIES

- BIS691, Generalized Linear Models
  Department of Biostatistics, Yale School of Public Health
  Spring 2020–2025
- BIS625, Categorical Data Analysis
  Department of Biostatistics, Yale School of Public Health
  Fall 2011–2017, Spring 2019
- Applied Data Science
  Department of Biological Sciences, Shanghai Jiao Tong University
  Spring 2023
- Longitudinal and Multilevel Data Analysis
  Department of Biological Sciences, Shanghai Jiao Tong University
  Spring 2017, 2018, 2021
- Generalized Linear Models
  Department of Biological Sciences, Shanghai Jiao Tong University
  Spring 2017

- Short course on Categorical Data Analysis
  Beijing Forestry University
  October 2012
- Short course on Nonparametric Statistics
  Beijing Forestry University
  October 2012
- STAT 220, Statistical Methods and Applications
  Department of Statistics, University of Chicago
  Spring 2008

MENTORING ACTIVITIES

- Postdoctoral/Research Associate Mentor
  - Zhong Wang (2013–2014, Professor at Dalian University of Technology)
  - Xinyu Zhang (joint with Ke Xu; 2014–2015, Research Scientist at Yale University)
  - Xiayuan Huang (2022–present)
  - Gang Xu (joint with Donna Spiegelman; 2023–present)
- PhD Dissertation Advisor
  - Weimiao Wu (Biostatistics, 2016–2021, First job: Meta Platforms, Inc.)
  - Ningshan Li (Bioinformatics & Biostatistics, Shanghai Jiao Tong University, 2019–2022, Postdoc at the Second Affiliated Hospital of the Chinese University of Hong Kong, Shenzhen)
  - Yunqing Liu (Biostatistics, joint with Xiting Yan; 2018–2023, First job: Food and Drug Administration)
  - Yi Dai (Biostatistics, 2022–present)
  - Xiao Xiao (Biostatistics, 2023–present)
- Master Thesis Advisor
  - Gongyi Wang (Biostatistics MS, 2013, First job: Michael Allen Co.)
  - Yun Huang (Biostatistics MS, 2014)
  - Xiyang Dou (Biostatistics MS, 2015, First job: HSBC)
  - Bingbing Lu (Biostatistics MS, 2015, First job: State Street Co.)
  - Siwan Huang (Biostatistics MS, 2016, First job: PwC)
  - Tiange Chen (Biostatistics MPH, 2016, **BIS master thesis award**, First job: IBM Research China)
  - Yuhao Qian (Environmental Health Sciences MPH, 2016, First job: Haoyue Capital)
  - Yunqing Liu (Biostatistics MS, 2018, **BIS master thesis award**, PhD student at Yale University)
  - Ningya Wang (Biostatistics MS, 2022, PhD student at Rutgers University)
  - Yi Dai (Biostatistics MPH, 2022, **BIS master thesis award**, PhD student at Yale University)

  - Nating Wang (Biostatistics MPH, 2023, PhD student at Cornell University)
- PhD Dissertation Committee
  - Jieming Chen (Computational Biology and Bioinformatics, 2015)
  - Josefa Martinez (Chronic Disease Epidemiology, 2016)
  - Qiongshi Lu (Biostatistics, 2017)
  - Christopher Fragoso (Computational Biology and Bioinformatics, 2017)
  - Qian Wang (Computational Biology and Bioinformatics, 2017)
  - Yasmmyn Salinas (Chronic Disease Epidemiology, 2019)
  - Mo Li (Biostatistics, 2020)
  - Boyang Li (Biostatistics, 2022)
  - Xing Wu (Molecular, Cellular and Developmental Biology, 2022)
  - Hongyu Li (Biostatistics, 2023)
  - Yuhan Xie (Biostatistics, 2023)
  - Zicheng Li (Chronic Disease Epidemiology, 2023)
  - Zihan Dong (Biostatistics, 2024)
  - Paulina Tolosa-Tort (Chronic Disease Epidemiology, 2024)
  - Biqing Zhu (Computational Biology and Bioinformatics, 2024)
  - Youshu Cheng (Biostatistics, expected in 2025)
  - Chen Lin (Biostatistics, expected in 2025)
  - Esther Kang (Chronic Disease Epidemiology, expected in 2027)
  - Zexiang Li (Biostatistics, expected in 2027)
- PhD Dissertation Reader
  - Gregory Ryslik (Biostatistics, 2014)
  - Qing Zhao (Biostatistics, 2015)
  - Zhixuan Fu (Biostatistics, 2016)
  - Tianqi Liu (Biostatistics, 2017)
  - Jiehuan Sun (Biostatistics, 2017)
  - Yiyi Liu (Biostatistics, 2018)
  - Li Zeng (Biostatistics, 2018)
  - Kyaw Sint (Biostatistics, 2019)
  - Megan Cahill (Epidemiology of Microbial Diseases, 2019)
  - Xiaoxuan Cai (Biostatistics, 2020)
  - Xiaochen Wang (Biostatistics, 2020)
  - Ming Chen (Biostatistics, 2021)
  - Wenxuan Deng (Biostatistics, 2021)
  - Daiwei Tang (Biostatistics, 2021)
  - Yaqing Xu (Biostatistics, 2021)
  - Huangdi Yi (Biostatistics, 2021)

  - Yiliang Zhang (Biostatistics, 2022)
  - Wei Dai (Biostatistics, 2023)
  - Chang Su (Biostatistics, 2023)
  - Shiying Wang (Biostatistics, 2023)
  - Yuge Wang (Biostatistics, 2023)
  - Chi Zhang (Biostatistics, 2024)
- PhD Qualifying Oral Exam Committee
  - Ming Chen (Biostatistics, 2018)
  - Boyang Li (Biostatistics, 2018)
  - Hongyu Li (Biostatistics, 2020)
  - Chang Su (Biostatistics, 2020)
  - Yuhan Xie (Biostatistics, 2020)
  - Youshu Cheng (Biostatistics, 2022)
  - Zihan Dong (Biostatistics, 2022)
  - Biqing Zhu (Computational Biology and Bioinformatics, 2022)
  - Wangjie Zheng (Biostatistics, 2023)
  - Zexiang Li (Biostatistics, 2024)
  - Xinning Shan (Biostatistics, 2024)
- Master Thesis Reader
  - Motao Sun (Chronic Disease Epidemiology MPH, 2016)
  - Yi Jin (Chronic Disease Epidemiology MPH, 2020)
- Research Assistants Supervised
  - Lu Wang (Biostatistics MS, Summer 2013, PhD student at University of Pennsylvania)
  - Zhaolong Yu (Computational Biology & Bioinformatics, Spring 2017)
  - Shiyu Wang (Biostatistics MS, 2018–2019, PhD student at Emory University)
  - Qile Dai (Biostatistics MS, 2018–2020, PhD student at Emory University)
  - Ran Tu (Biostatistics MPH, 2020–2021, PhD student at Georgetown University)
  - Wenjing Li (Statistics, University of Nevada, Las Vegas, 2018–2021)
  - Gang Xu (Statistics, University of Nevada, Las Vegas, 2018–2022)
  - Wenhao Jiang (Biostatistics MS, 2022–2023, PhD student at the University of Massachusetts Amherst)
  - Ji Qi (Biostatistics MS, 2021–2023, PhD student at the Chinese University of Hong Kong)
  - Jiayi Zhao (Biostatistics MS, 2021–2023, Postgraduate Associate at Yale University)
  - Linchuan Shen (Statistics, University of Nevada, Las Vegas, 2018–2024, Instructor at University of Nevada, Las Vegas)
  - Yihan Liu (Biostatistics MS, 2023–2024, PhD student at Yale University)

  - Annie Jiang (Biostatistics MPH, Summer 2023)
- Visiting Scholar Mentor
  - Lihong Zhao (Visiting PhD Student, Beijing University of Chinese Medicine, 2012–2013)
  - Meng Xu (Visiting Associate Professor, Nanjing Forestry University, 2014–2015)
  - Yisha Tang (Undergraduate, University of Science & Technology of China, Summer 2018)
  - Nayang Shan (Visiting PhD Student, Tsinghua University, 2019–2020)
  - Huanhuan Wei (Visiting PhD Student, Shanghai Jiao Tong University, 2022–2023)
  - Yao Lu (Visiting PhD Student, Tsinghua University, 2024–present)